

ABSTRACT

The present invention relates to genetic mapping of complex quantitative and qualitative traits. This invention more particularly relates to methods to identify identical DNA fragments from two different DNA sources. The method allows the amplification of the DNAs, their labelling, and the separation of perfectly matched DNAs from imperfectly matched DNAs or from DNAs formed through hybridisation from the same source (e.g., homohybrids). The invention can be used to identify genes or gene mutations, which are relevant to pathological conditions or particular traits.